



PCDMOD~11.TXT
SEQUENCE LISTING

<110> Elena, Babiychuk

Sergei, Kushnir

Marc, De Block

<120> Methods and means to modulate programmed cell death in eukaryotic cells

<130> 58764.0000039

<140> US 10/705,197

<141> 2003-11-12

<150> US 09/118,276

<151> 1998-07-11

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 3211

<212> DNA

<213> Zea mays

PCDMOD~11.TXT

<220>

<221> CDS

<222> (113) .. (3022)

<223>

<400> 1
acctacacctga atacgtcatc cctaagtgtt ccgcattcctc tgcgtccgg cctccaaactc
60

catcgaaggg gctagggaga ggagggaaacc cgaaccacag caggccggcg ca atg gcg
118

Met Ala

1

gcg ccg cca aag gcg tgg aag gcg gag tat gcc aag tct ggg cgg gcc
166
Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly Arg Ala

5

10

15

tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc cgt ctt
214
Ser Cys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu Arg Leu

20

25

30

ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg atg tgg
262
Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro Met Trp

35

40

45

50

aac cat gcc agc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg
310
Asn His Ala Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp

PCDMOD~11.TXT

55

60

65

gat gat caa gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt
358
Asp Asp Gln Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly

70

75

80

aca agt tct aca gct gct cct gag aaa tgt aca att gag att gct
406
Thr Ser Ser Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala

85

90

95

cca tct gcc cgt act tca tgt aga cga tgc agt gaa aag att aca aaa
454
Pro Ser Ala Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys

100

105

110

gga tcg gtc cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt
502
Gly Ser Val Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly

115

120

125

130

ata cca tgg tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca
550
Ile Pro Trp Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala

135

140

145

act gtt gag aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag
598
Thr Val Glu Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys

150

155

160

aga acc atg ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa
646

PCDMOD~11.TXT

Arg Thr Met Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln

165

170

175

aat aag ggt tcc aag cgc aag aaa agt gaa aat gat att gat agc tac
694

Asn Lys Gly Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr

180

185

190

aaa tcc gcc agg tta gat gaa agt aca tct gaa ggt aca gtg cga aac
742

Lys Ser Ala Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn

195

200

205

210

aaa ggg caa ctt gta gac cca cgt ggt tcc aat act agt tca gct gat
790

Lys Gly Gln Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp

215

220

225

atc caa cta aag ctt aag gag caa agt gac aca ctt tgg aag tta aag
838

Ile Gln Leu Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys

230

235

240

gat gga ctt aag act cat gta tcg gct gct gaa tta agg gat atg ctt
886

Asp Gly Leu Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu

245

250

255

gag gct aat ggg cag gat aca tca gga cca gaa agg cac cta ttg gat
934

Glu Ala Asn Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp

260

265

270

cgc tgt gcg gat gga atg ata ttt gga gcg ctg ggt cct tgc cca gtc

PCDMOD~11.TXT

982

Arg Cys Ala Asp Gly Met Ile Phe Gly Ala Leu Gly Pro Cys Pro Val

275

280

285

290

tgt gct aat ggc atg tac tat tat aat ggt cag tac caa tgc agt ggt
1030

Cys Ala Asn Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly

295

300

305

aat gtg tca gag tgg tcc aag tgt aca tac tct gcc aca gaa cct gtc
1078

Asn Val Ser Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val

310

315

320

cgc gtt aag aag aag tgg caa att cca cat gga aca aag aat gat tac
1126

Arg Val Lys Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr

325

330

335

ctt atg aag tgg ttc aaa tct caa aag gtt aag aaa cca gag agg gtt
1174

Leu Met Lys Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val

340

345

350

ctt cca cca atg tca cct gag aaa tct gga agt aaa gca act cag aga
1222

Leu Pro Pro Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg

355

360

365

370

aca tca ttg ctg tct tct aaa ggg ttg gat aaa tta agg ttt tct gtt
1270

Thr Ser Leu Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val

375

380

385

PCDMOD~11.TXT

gta gga caa tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa
1318
Val Gly Gln Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys

390 395 400

ctt gct ggt gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt
1366
Leu Ala Gly Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys

405 410 415

tta att gca tgt ggt gag ctc gac aat gaa aat gct gaa gtc agg aaa
1414
Leu Ile Ala Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys

420 425 430

gca agg agg ctg aag ata cca att gta agg gag ggt tac att gga gaa
1462
Ala Arg Arg Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu

435 440 445 450

tgt gtt aaa aag aac aaa atg ctg cca ttt gat ttg tat aaa cta gag
1510
Cys Val Lys Lys Asn Lys Met Leu Pro Phe Asp Leu Tyr Lys Leu Glu

455 460 465

aat gcc tta gag tcc tca aaa ggc agt act gtc act gtt aaa gtt aag
1558
Asn Ala Leu Glu Ser Ser Lys Gly Ser Thr Val Thr Val Lys Val Lys

470 475 480

ggc cga agt gct gtt cat gag tcc tct ggt ttg caa gat act gct cac
1606
Gly Arg Ser Ala Val His Glu Ser Ser Gly Leu Gln Asp Thr Ala His

485 490 495

PCDMOD~11.TXT

att ctt gaa gat ggg aaa agc ata tac aat gca acc tta aac atg tct
1654
Ile Leu Glu Asp Gly Lys Ser Ile Tyr Asn Ala Thr Leu Asn Met Ser

500 505 510

gac ctg gca cta ggt gtg aac agc tac tat gta ctc cag atc att gaa
1702
Asp Leu Ala Leu Gly Val Asn Ser Tyr Tyr Val Leu Gln Ile Ile Glu

515 520 525 530

cag gat gat ggg tct gag tgc tac gta ttt cgt aag tgg gga cgg gtt
1750
Gln Asp Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val

535 540 545

ggg agt gag aaa att gga ggg caa aaa ctg gag gag atg tca aaa act
1798
Gly Ser Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr

550 555 560

gag gca atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac
1846
Glu Ala Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn

565 570 575

tca tgg gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct ggg
1894
Ser Trp Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly

580 585 590

aga ttt tac cca ctt gat gtt gat tat ggt gtt aag aaa gca cca aaa
1942
Arg Phe Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys

595 600 605 610

PCDMOD~11.TXT

cgg aaa gat atc agt gaa atg aaa agt tct ctt gct cct caa ttg cta
1990
Arg Lys Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu

615 620 625

gaa ctc atg aag atg ctt ttc aat gtg gag aca tat aga gct gct atg
2038
Glu Leu Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met

630 635 640

atg gaa ttt gaa att aat atg tca gaa atg cct ctt ggg aag cta agc
2086
Met Glu Phe Glu Ile Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser

645 650 655

aag gaa aat att gag aaa gga ttt gaa gca tta act gag ata cag aat
2134
Lys Glu Asn Ile Glu Lys Gly Phe Glu Ala Leu Thr Glu Ile Gln Asn

660 665 670

tta ttg aag gac acc gct gat caa gca ctg gct gtt aga gaa agc tta
2182
Leu Leu Lys Asp Thr Ala Asp Gln Ala Leu Ala Val Arg Glu Ser Leu

675 680 685 690

att gtt gct gcg agc aat cgc ttt ttc act ctt atc cct tct att cat
2230
Ile Val Ala Ala Ser Asn Arg Phe Phe Thr Leu Ile Pro Ser Ile His

695 700 705

cct cat att ata cgg gat gag gat gat ttg atg atc aaa gcg aaa atg
2278
Pro His Ile Ile Arg Asp Glu Asp Asp Leu Met Ile Lys Ala Lys Met

PCDMOD~11.TXT

710

715

720

ctt gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc
 2326

Leu Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe

725

730

735

gat agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac
 2374

Asp Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His

740

745

750

tgt gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att
 2422

Cys Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile

755

760

765

770

gag cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcg
 2470

Glu Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser

775

780

785

ctg gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat
 2518

Leu Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn

790

795

800

aag tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg
 2566

Lys Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp

805

810

815

cac ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta
 2614

His Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu

PCDMOD~11.TXT

820

825

830

aga att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa
2662
Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys

835

840

845

850

ggc ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat
2710
Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr

855

860

865

gtg gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct
2758
Val Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala

870

875

880

tta gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct
2806
Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro

885

890

895

cca aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg
2854
Pro Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu

900

905

910

gag tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc
2902
Glu Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly

915

920

925

930

aag ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag
2950

PCDMOD~11.TXT

Lys Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu

935

940

945

tac atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag

2998

Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys

950

955

960

gtg cgt ttc cat cac aag agg tag ctggagact aggcaagtag agttggaagg

3052

Val Arg Phe His His Lys Arg

965

tagagaagca gagtaggcg atgcctcttt tggattattt agtaagcctg gcatgtattt

3112

atgggtgctc gcgcttgcac cattttggta agtgttgctt gggcatcagc gcgaatagca

3172

ccaatcacac acttttacct aatgacgttt tactgtata

3211

<210> 2

<211> 969

<212> PRT

<213> Zea mays

<400> 2

Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
1 5 10 15

Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
20 25 30

PCDMOD~11.TXT

Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45

Met Trp Asn His Ala Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu
50 55 60

Arg Trp Asp Asp Gln Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser
65 70 75 80

Ala Gly Thr Ser Ser Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu
85 90 95

Ile Ala Pro Ser Ala Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile
100 105 110

Thr Lys Gly Ser Val Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro
115 120 125

Lys Gly Ile Pro Trp Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro
130 135 140

Ser Ala Thr Val Glu Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu
145 150 155 160

Asp Lys Arg Thr Met Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn
165 170 175

Glu Gln Asn Lys Gly Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp
180 185 190

Ser Tyr Lys Ser Ala Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val
195 200 205

Arg Asn Lys Gly Gln Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser
210 215 220

PCDMOD~11.TXT

Ala Asp Ile Gln Leu Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys
225 230 235 240

Leu Lys Asp Gly Leu Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp
245 250 255

Met Leu Glu Ala Asn Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu
260 265 270

Leu Asp Arg Cys Ala Asp Gly Met Ile Phe Gly Ala Leu Gly Pro Cys
275 280 285

Pro Val Cys Ala Asn Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys
290 295 300

Ser Gly Asn Val Ser Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu
305 310 315 320

Pro Val Arg Val Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn
325 330 335

Asp Tyr Leu Met Lys Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu
340 345 350

Arg Val Leu Pro Pro Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr
355 360 365

Gln Arg Thr Ser Leu Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe
370 375 380

Ser Val Val Gly Gln Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys
385 390 395 400

Leu Lys Leu Ala Gly Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile
405 410 415

PCDMOD~11.TXT

Asp Cys Leu Ile Ala Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val
420 425 430

Arg Lys Ala Arg Arg Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile
435 440 445

Gly Glu Cys Val Lys Lys Asn Lys Met Leu Pro Phe Asp Leu Tyr Lys
450 455 460

Leu Glu Asn Ala Leu Glu Ser Ser Lys Gly Ser Thr Val Thr Val Lys
465 470 475 480

Val Lys Gly Arg Ser Ala Val His Glu Ser Ser Gly Leu Gln Asp Thr
485 490 495

Ala His Ile Leu Glu Asp Gly Lys Ser Ile Tyr Asn Ala Thr Leu Asn
500 505 510

Met Ser Asp Leu Ala Leu Gly Val Asn Ser Tyr Tyr Val Leu Gln Ile
515 520 525

Ile Glu Gln Asp Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly
530 535 540

Arg Val Gly Ser Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser
545 550 555 560

Lys Thr Glu Ala Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr
565 570 575

Gly Asn Ser Trp Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln
580 585 590

Pro Gly Arg Phe Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala
595 600 605

PCDMOD~11.TXT

Pro Lys Arg Lys Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln
610 615 620

Leu Leu Glu Leu Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala
625 630 635 640

Ala Met Met Glu Phe Glu Ile Asn Met Ser Glu Met Pro Leu Gly Lys
645 650 655

Leu Ser Lys Glu Asn Ile Glu Lys Gly Phe Glu Ala Leu Thr Glu Ile
660 665 670

Gln Asn Leu Leu Lys Asp Thr Ala Asp Gln Ala Leu Ala Val Arg Glu
675 680 685

Ser Leu Ile Val Ala Ala Ser Asn Arg Phe Phe Thr Leu Ile Pro Ser
690 695 700

Ile His Pro His Ile Ile Arg Asp Glu Asp Asp Leu Met Ile Lys Ala
705 710 715 720

Lys Met Leu Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val
725 730 735

Gly Phe Asp Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys
740 745 750

Leu His Cys Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys
755 760 765

Leu Ile Glu Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp
770 775 780

Trp Ser Leu Glu Leu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu
785 790 795 800

PCDMOD~11.TXT

Leu Asn Lys Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu
805 810 815

Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln
820 825 830

Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe
835 840 845

Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr
850 855 860

Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu
865 870 875 880

Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp
885 890 895

Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val
900 905 910

Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro
915 920 925

Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr
930 935 940

Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu
945 950 955 960

Leu Lys Val Arg Phe His His Lys Arg
965

<210> 3

<211> 2295

PCDMOD~11.TXT

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (107) .. (2068)

<223>

<400> 3

tgacctgttc catcccgcca gcccttccgc tcccacgacc caacccact gcccgagcc
60

cccgagcctt ctcgaatctt gcgagaaccc caggggcgag gagcag atg tcg gcg
115

Met Ser Ala ,

1

agg cta cgg gtg gcg gac gtc cgc gcg gag ctt cag cgc cgc ggc ctc
163

Arg Leu Arg Val Ala Asp Val Arg Ala Glu Leu Gln Arg Arg Gly Leu

5

10

15

gat gta tcc ggc acc aag cct gct ctc gtg cgg agg ctg gac gcc gca
211

Asp Val Ser Gly Thr Lys Pro Ala Leu Val Arg Arg Leu Asp Ala Ala

20

25

30

35

att tgc gag gcg gag aag gcc gtg gtg gct gct gcg cca acc agt gtg
259

Ile Cys Glu Ala Glu Lys Ala Val Val Ala Ala Ala Pro Thr Ser Val

40

45

50

PCDMOD~11.TXT

gca aat ggg tat gac gta gcc gta gat ggc aaa agg aac tgc ggg aat
307
Ala Asn Gly Tyr Asp Val Ala Val Asp Gly Lys Arg Asn Cys Gly Asn

55

60

65

aat aag agg aaa agg tcc ggg gat ggg ggt gaa gag gga aac ggc gat
355
Asn Lys Arg Lys Arg Ser Gly Asp Gly Gly Glu Glu Gly Asn Gly Asp

70

75

80

acg tgt aca gat gtg aca aaa cta gag ggc atg agc tat cgt gag ctg
403
Thr Cys Thr Asp Val Thr Lys Leu Glu Gly Met Ser Tyr Arg Glu Leu

85

90

95

cag gga ttg gcc aag gca cgt gga gtt gcg gca aat ggg ggc aag aaa
451
Gln Gly Leu Ala Lys Ala Arg Gly Val Ala Ala Asn Gly Lys Lys

100

105

110

115

gat gtt atc cag agg ttg ctc tcg gcg act gct ggt cct gct gca gtt
499
Asp Val Ile Gln Arg Leu Leu Ser Ala Thr Ala Gly Pro Ala Ala Val

120

125

130

gca gat ggt ggt cct ctg ggc gcc aag gaa gtc ata aaa ggt ggt gat
547
Ala Asp Gly Gly Pro Leu Gly Ala Lys Glu Val Ile Lys Gly Gly Asp

135

140

145

gag gag gtt gag gtg aaa aag gag aag atg gtt act gcc acg aag aag
595
Glu Glu Val Glu Val Lys Lys Glu Lys Lys Met Val Thr Ala Thr Lys Lys

150

155

160

PCDMOD~11.TXT

gga gct gca gtg ctg gat cag cac att ccc gat cac ata aaa gtg aac
643
Gly Ala Ala Val Leu Asp Gln His Ile Pro Asp His Ile Lys Val Asn

165 170 175

tat cat gtc ttg caa gtg ggc gat gaa atc tat gat gcc acc ttg aac
691
Tyr His Val Leu Gln Val Gly Asp Glu Ile Tyr Asp Ala Thr Leu Asn

180 185 190 195

cag act aat gtt gga gac aac aac aat aag ttc tat atc att caa gtt
739
Gln Thr Asn Val Gly Asp Asn Asn Lys Phe Tyr Ile Ile Gln Val

200 205 210

tta gaa tct gat gct ggt gga agc ttt atg gtt tac aat aga tgg gga
787
Leu Glu Ser Asp Ala Gly Gly Ser Phe Met Val Tyr Asn Arg Trp Gly

215 220 225

aga gtt ggg gta cga ggt caa gat aaa cta cat ggt ccc tcc cca aca
835
Arg Val Gly Val Arg Gly Gln Asp Lys Leu His Gly Pro Ser Pro Thr

230 235 240

cga gac caa gca ata tat gaa ttt gag ggg aag ttc cac aac aaa acc
883
Arg Asp Gln Ala Ile Tyr Glu Phe Glu Gly Lys Phe His Asn Lys Thr

245 250 255

aat aat cat tgg tct gat cgc aag aac ttc aaa tgt tat gca aag aaa
931
Asn Asn His Trp Ser Asp Arg Lys Asn Phe Lys Cys Tyr Ala Lys Lys

PCDMOD~11.TXT

260

265

270

275

tac act tgg ctt gaa atg gat tat ggt gaa act gag aaa gaa ata gag
 979
 Tyr Thr Trp Leu Glu Met Asp Tyr Gly Glu Thr Glu Lys Glu Ile Glu

280

285

290

aaa ggt tcc att act gat cag ata aaa gag aca aaa ctt gaa act aga
 1027
 Lys Gly Ser Ile Thr Asp Gln Ile Lys Glu Thr Lys Leu Glu Thr Arg

295

300

305

att gcg cag ttc ata tcc ctg atc tgc aat att agc atg atg aag caa
 1075
 Ile Ala Gln Phe Ile Ser Leu Ile Cys Asn Ile Ser Met Met Lys Gln

310

315

320

aga atg gtg gaa ata ggt tat aat gct gaa aag ctt ccc ctt gga aag
 1123
 Arg Met Val Glu Ile Gly Tyr Asn Ala Glu Lys Leu Pro Leu Gly Lys

325

330

335

cta agg aaa gct aca ata ctt aag ggt tat cat gtt ttg aaa agg ata
 1171
 Leu Arg Lys Ala Thr Ile Leu Lys Gly Tyr His Val Leu Lys Arg Ile

340

345

350

355

tcc gat gtt att tca aag gcg gac agg aga cat ctt gag caa ttg act
 1219
 Ser Asp Val Ile Ser Lys Ala Asp Arg Arg His Leu Glu Gln Leu Thr

360

365

370

ggg gaa ttc tac acc gtg att cct cat gac ttt ggt ttc aga aag atg
 1267
 Gly Glu Phe Tyr Thr Val Ile Pro His Asp Phe Gly Phe Arg Lys Met

PCDMOD~11.TXT

375

380

385

cgt gaa ttt att atc gat act cct cag aaa cta aaa gct aag ctg gag
1315
Arg Glu Phe Ile Ile Asp Thr Pro Gln Lys Leu Lys Ala Lys Leu Glu

390

395

400

atg gtt gaa gcc ctt ggt gag att gaa att gca act aaa ctt ttg gag
1363
Met Val Glu Ala Leu Gly Glu Ile Glu Ile Ala Thr Lys Leu Leu Glu

405

410

415

gat gat tca agt gac cag gat gat ccg ttg tat gct cga tac aag caa
1411
Asp Asp Ser Ser Asp Gln Asp Asp Pro Leu Tyr Ala Arg Tyr Lys Gln

420

425

430

435

ctt cat tgt gat ttc aca cct ctt gaa gct gat tca gat gag tac tct
1459
Leu His Cys Asp Phe Thr Pro Leu Glu Ala Asp Ser Asp Glu Tyr Ser

440

445

450

atg ata aaa tca tat ttg aga aat aca cat gga aaa aca cac tct ggt
1507
Met Ile Lys Ser Tyr Leu Arg Asn Thr His Gly Lys Thr His Ser Gly

455

460

465

tat acg gtg gac ata gtg caa ata ttt aag gtt tca agg cat ggt gaa
1555
Tyr Thr Val Asp Ile Val Gln Ile Phe Lys Val Ser Arg His Gly Glu

470

475

480

aca gag cga ttt caa aaa ttt gct agt aca aga aat agg atg ctt ttg
1603

PCDMOD~11.TXT

Thr Glu Arg Phe Gln Lys Phe Ala Ser Thr Arg Asn Arg Met Leu Leu

485

490

495

tgg cat ggt tct cgg ttg agc aac tgg gct ggg atc ctt tct cag ggt
1651

Trp His Gly Ser Arg Leu Ser Asn Trp Ala Gly Ile Leu Ser Gln Gly

500

505

510

515

ctg cga atc gct cct cct gaa gca cct gtt act ggt tac atg ttt ggc
1699

Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly

520

525

530

aag ggt gtt tac ttt gct gac atg ttt tca aag agt gca aac tat tgc
1747

Lys Gly Val Tyr Phe Ala Asp Met Phe Ser Lys Ser Ala Asn Tyr Cys

535

540

545

tac gcc tct gaa gca tgt aga tct gga gta ctg ctt tta tgt gag gtt
1795

Tyr Ala Ser Glu Ala Cys Arg Ser Gly Val Leu Leu Leu Cys Glu Val

550

555

560

gca ttg ggc gat atg aat gag cta ctg aat gca gat tac gat gct aat
1843

Ala Leu Gly Asp Met Asn Glu Leu Leu Asn Ala Asp Tyr Asp Ala Asn

565

570

575

aac ctg ccc aaa gga aaa tta aga tcc aag gga gtt ggt caa aca gca
1891

Asn Leu Pro Lys Gly Lys Leu Arg Ser Lys Gly Val Gly Gln Thr Ala

580

585

590

595

cct aac atg gtc gag tct aag gtc gct gac gat ggt gtt gtt ccc

PCDMOD~11.TXT

1939

Pro Asn Met Val Glu Ser Lys Val Ala Asp Asp Gly Val Val Val Pro

600

605

610

ctt ggc gaa ccc aaa cag gaa cct tcc aaa agg ggt ggc ttg ctt tat
1987

Leu Gly Glu Pro Lys Gln Glu Pro Ser Lys Arg Gly Gly Leu Leu Tyr

615

620

625

aat gag tac ata gtg tac aac gta gac cag ata aga atg cggtat gtc
2035

Asn Glu Tyr Ile Val Tyr Asn Val Asp Gln Ile Arg Met Arg Tyr Val

630

635

640

tta cat gtt aac ttc aat ttc aag aga cggtatgttgcggaaac
2088

Leu His Val Asn Phe Asn Phe Lys Arg Arg

645

650

tgttgctgag atcttagcag aacatatgtg gacttatagc accaggtgcc ctcagcctca
2148

ttttctgagc aaatttggta gccttgcatttcgatttg gttcagctt ctagccccat
2208

tgtatgattga tactgagtgt atatatgaac cattgatatac caccttccat gtacttaagt
2268

tttttaaca tgtcccatgc ataataa

2295

<210> 4

<211> 653

<212> PRT

<213> Zea mays

PCDMOD~11.TXT

<400> 4

Met Ser Ala Arg Leu Arg Val Ala Asp Val Arg Ala Glu Leu Gln Arg
1 5 10 15

Arg Gly Leu Asp Val Ser Gly Thr Lys Pro Ala Leu Val Arg Arg Leu
20 25 30

Asp Ala Ala Ile Cys Glu Ala Glu Lys Ala Val Val Ala Ala Ala Pro
35 40 45

Thr Ser Val Ala Asn Gly Tyr Asp Val Ala Val Asp Gly Lys Arg Asn
50 55 60

Cys Gly Asn Asn Lys Arg Lys Arg Ser Gly Asp Gly Gly Glu Gly
65 70 75 80

Asn Gly Asp Thr Cys Thr Asp Val Thr Lys Leu Glu Gly Met Ser Tyr
85 90 95

Arg Glu Leu Gln Gly Leu Ala Lys Ala Arg Gly Val Ala Ala Asn Gly
100 105 110

Gly Lys Lys Asp Val Ile Gln Arg Leu Leu Ser Ala Thr Ala Gly Pro
115 120 125

Ala Ala Val Ala Asp Gly Gly Pro Leu Gly Ala Lys Glu Val Ile Lys
130 135 140

Gly Gly Asp Glu Glu Val Glu Val Lys Lys Glu Lys Lys Met Val Thr Ala
145 150 155 160

Thr Lys Lys Gly Ala Ala Val Leu Asp Gln His Ile Pro Asp His Ile
165 170 175

PCDMOD~11.TXT

Lys Val Asn Tyr His Val Leu Gln Val Gly Asp Glu Ile Tyr Asp Ala
180 185 190

Thr Leu Asn Gln Thr Asn Val Gly Asp Asn Asn Asn Lys Phe Tyr Ile
195 200 205

Ile Gln Val Leu Glu Ser Asp Ala Gly Gly Ser Phe Met Val Tyr Asn
210 215 220

Arg Trp Gly Arg Val Gly Val Arg Gly Gln Asp Lys Leu His Gly Pro
225 230 235 240

Ser Pro Thr Arg Asp Gln Ala Ile Tyr Glu Phe Glu Gly Lys Phe His
245 250 255

Asn Lys Thr Asn Asn His Trp Ser Asp Arg Lys Asn Phe Lys Cys Tyr
260 265 270

Ala Lys Lys Tyr Thr Trp Leu Glu Met Asp Tyr Gly Glu Thr Glu Lys
275 280 285

Glu Ile Glu Lys Gly Ser Ile Thr Asp Gln Ile Lys Glu Thr Lys Leu
290 295 300

Glu Thr Arg Ile Ala Gln Phe Ile Ser Leu Ile Cys Asn Ile Ser Met
305 310 315 320

Met Lys Gln Arg Met Val Glu Ile Gly Tyr Asn Ala Glu Lys Leu Pro
325 330 335

Leu Gly Lys Leu Arg Lys Ala Thr Ile Leu Lys Gly Tyr His Val Leu
340 345 350

Lys Arg Ile Ser Asp Val Ile Ser Lys Ala Asp Arg Arg His Leu Glu
355 360 365

PCDMOD~11.TXT

Gln Leu Thr Gly Glu Phe Tyr Thr Val Ile Pro His Asp Phe Gly Phe
370 375 380

Arg Lys Met Arg Glu Phe Ile Ile Asp Thr Pro Gln Lys Leu Lys Ala
385 390 395 400

Lys Leu Glu Met Val Glu Ala Leu Gly Glu Ile Glu Ile Ala Thr Lys
405 410 415

Leu Leu Glu Asp Asp Ser Ser Asp Gln Asp Asp Pro Leu Tyr Ala Arg
420 425 430

Tyr Lys Gln Leu His Cys Asp Phe Thr Pro Leu Glu Ala Asp Ser Asp
435 440 445

Glu Tyr Ser Met Ile Lys Ser Tyr Leu Arg Asn Thr His Gly Lys Thr
450 455 460

His Ser Gly Tyr Thr Val Asp Ile Val Gln Ile Phe Lys Val Ser Arg
465 470 475 480

His Gly Glu Thr Glu Arg Phe Gln Lys Phe Ala Ser Thr Arg Asn Arg
485 490 495

Met Leu Leu Trp His Gly Ser Arg Leu Ser Asn Trp Ala Gly Ile Leu
500 505 510

Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr
515 520 525

Met Phe Gly Lys Gly Val Tyr Phe Ala Asp Met Phe Ser Lys Ser Ala
530 535 540

Asn Tyr Cys Tyr Ala Ser Glu Ala Cys Arg Ser Gly Val Leu Leu Leu
545 550 555 560

PCDMOD~11.TXT

Cys Glu Val Ala Leu Gly Asp Met Asn Glu Leu Leu Asn Ala Asp Tyr
565 570 575

Asp Ala Asn Asn Leu Pro Lys Gly Lys Leu Arg Ser Lys Gly Val Gly
580 585 590

Gln Thr Ala Pro Asn Met Val Glu Ser Lys Val Ala Asp Asp Gly Val
 595 600 605

Val Val Pro Leu Gly Glu Pro Lys Gln Glu Pro Ser Lys Arg Gly Gly
610 615 620

Leu Leu Tyr Asn Glu Tyr Ile Val Tyr Asn Val Asp Gln Ile Arg Met
625 630 635 640

Arg Tyr Val Leu His Val Asn Phe Asn Phe Lys Arg Arg
645 650

<210> 5

<211> 2147

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (129) .. (2042)

<223>-

<400> 5

attgatgaag aagaaaacga agaagaagac tcttcaaatg ctcgcgcgaa ctcaacttctg
60

PCDMOD~11.TXT

acgaaaacca tacttcctca gtctcattcc ctttccgacg aactattctc ctgaagaaga
120

agacgaaa atg gcg aac aag ctc aaa gtc gac gaa ctc cgt tta aaa ctc
170

Met Ala Asn Lys Leu Lys Val Asp Glu Leu Arg Leu Lys Leu

1 5 10

gcc gag cgt gga ctc agt act act gga gtc aaa gcc gtt ctg gtg gag
218

Ala Glu Arg Gly Leu Ser Thr Thr Gly Val Lys Ala Val Leu Val Glu

15 20 25 30

agg ctt gaa gag gct atc gca gaa gac act aag aag gaa gaa tca aag
266

Arg Leu Glu Glu Ala Ile Ala Glu Asp Thr Lys Lys Glu Glu Ser Lys

35 40 45

agc aag agg aaa aga aat tct tct aat gat act tat gaa tcg aac aaa
314

Ser Lys Arg Lys Arg Asn Ser Asn Asp Thr Tyr Glu Ser Asn Lys

50 55 60

ttg att gca att ggc gaa ttt cgt ggg atg att gtg aag gaa ttg cgt
362

Leu Ile Ala Ile Gly Glu Phe Arg Gly Met Ile Val Lys Glu Leu Arg

65 70 75

gag gaa gct att aag aga ggc tta gat aca aca gga acc aaa aag gat
410

Glu Glu Ala Ile Lys Arg Gly Leu Asp Thr Thr Gly Thr Lys Lys Asp

80 85 90

ctt ctt gag agg ctt tgc aat gat gct aat aac gtt tcc aat gca cca
458

Leu Leu Glu Arg Leu Cys Asn Asp Ala Asn Asn Val Ser Asn Ala Pro

PCDMOD~11.TXT

95 100 105 110
gtc aaa tcc agt aat ggg aca gat gaa gct gaa gat gac aac aat ggc
506
Val Lys Ser Ser Asn Gly Thr Asp Glu Ala Glu Asp Asp Asn Asn Gly
115 120 125
ttt gaa gaa gaa aag aaa gaa gag aaa atc gta acc gcg aca aag aag
554
Phe Glu Glu Glu Lys Lys Glu Glu Lys Ile Val Thr Ala Thr Lys Lys
130 135 140
ggc gca gcg gtg cta gat cag tgg att cct gat gag ata aag agt cag
602
Gly Ala Ala Val Leu Asp Gln Trp Ile Pro Asp Glu Ile Lys Ser Gln
145 150 155
tac cat gtt cta caa agg ggt gat gat gtt tat gat gct atc tta aat
650
Tyr His Val Leu Gln Arg Gly Asp Asp Val Tyr Asp Ala Ile Leu Asn
160 165 170
cag aca aat gtc agg gat aat aat aac aag ttc ttt gtc cta caa gtc
698
Gln Thr Asn Val Arg Asp Asn Asn Asn Lys Phe Phe Val Leu Gln Val
175 180 185 190
cta gag tcg gat agt aaa aag aca tac atg gtt tac act aga tgg gga
746
Leu Glu Ser Asp Ser Lys Lys Thr Tyr Met Val Tyr Thr Arg Trp Gly
195 200 205
aga gtt ggt gtg aaa gga caa agt aag cta gat ggg cct tat gac tca
794

PCDMOD~11.TXT

Arg Val Gly Val Lys Gly Gln Ser Lys Leu Asp Gly Pro Tyr Asp Ser

210

215

220

tgg gat cgt gcg ata gag ata ttt acc aat aag ttc aat gac aag aca
842

Trp Asp Arg Ala Ile Glu Ile Phe Thr Asn Lys Phe Asn Asp Lys Thr

225

230

235

aag aat tat tgg tct gac aga aag gag ttt atc cca cat ccc aag tcc
890

Lys Asn Tyr Trp Ser Asp Arg Lys Glu Phe Ile Pro His Pro Lys Ser

240

245

250

tat aca tgg ctc gaa atg gat tac gga aaa gag gaa aat gat tca ccg
938

Tyr Thr Trp Leu Glu Met Asp Tyr Gly Lys Glu Glu Asn Asp Ser Pro

255

260

265

270

gtc aat aat gat att ccg agt tca tct tcc gaa gtt aaa cct gaa caa
986

Val Asn Asn Asp Ile Pro Ser Ser Ser Glu Val Lys Pro Glu Gln

275

280

285

tca aaa cta gat act cgg gtt gcc aag ttc atc tct ctt ata tgt aat
1034

Ser Lys Leu Asp Thr Arg Val Ala Lys Phe Ile Ser Leu Ile Cys Asn

290

295

300

gtc agc atg atg gca cag cat atg atg gaa ata gga tat aac gct aac
1082

Val Ser Met Met Ala Gln His Met Met Glu Ile Gly Tyr Asn Ala Asn

305

310

315

aaa ttg cca ctc ggc aag ata agc aag tcc aca att tca aag ggt tat

PCDMOD~11.TXT

1130

Lys Leu Pro Leu Gly Lys Ile Ser Lys Ser Thr Ile Ser Lys Gly Tyr

320

325

330

gaa gtg ctg aag aga ata tcg gag gtg att gac cgg tat gat aga acg

1178

Glu Val Leu Lys Arg Ile Ser Glu Val Ile Asp Arg Tyr Asp Arg Thr

335

340

345

350

agg ctt gag gaa ctg agt gga gag ttc tac aca gtg ata cct cat gat

1226

Arg Leu Glu Glu Leu Ser Gly Glu Phe Tyr Thr Val Ile Pro His Asp

355

360

365

ttt ggt ttt aag aaa atg agt cag ttt gtt ata gac act cct caa aag

1274

Phe Gly Phe Lys Lys Met Ser Gln Phe Val Ile Asp Thr Pro Gln Lys

370

375

380

ttg aaa cag aaa att gaa atg gtt gaa gca tta ggt gaa att gaa ctc

1322

Leu Lys Gln Lys Ile Glu Met Val Glu Ala Leu Gly Glu Ile Glu Leu

385

390

395

gca aca aag ttg ttg tcc gtc gac ccg gga ttg cag gat gat cct tta

1370

Ala Thr Lys Leu Leu Ser Val Asp Pro Gly Leu Gln Asp Asp Pro Leu

400

405

410

tat tat cac tac cag caa ctt aat tgt ggt ttg acg cca gta gga aat

1418

Tyr Tyr His Tyr Gln Gln Leu Asn Cys Gly Leu Thr Pro Val Gly Asn

415

420

425

430

PCDMOD~11.TXT

gat tca gag gag ttc tct atg gtt gct aat tac atg gag aac act cat
1466
Asp Ser Glu Glu Phe Ser Met Val Ala Asn Tyr Met Glu Asn Thr His

435

440

445

gca aag acg cat tcg gga tat acg gtt gag att gcc caa cta ttt aga
1514
Ala Lys Thr His Ser Gly Tyr Thr Val Glu Ile Ala Gln Leu Phe Arg

450

455

460

gct tcg aga gct gtt gaa gct gat cga ttc caa cag ttt tca agt tcg
1562
Ala Ser Arg Ala Val Glu Ala Asp Arg Phe Gln Gln Phe Ser Ser

465

470

475

aag aac agg atg cta ctc tgg cac ggt tca cgt ctc act aac tgg gct
1610
Lys Asn Arg Met Leu Leu Trp His Gly Ser Arg Leu Thr Asn Trp Ala

480

485

490

ggt att tta tct caa ggt ctg cga ata gct cct cct gaa gcg cct gta
1658
Gly Ile Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val

495

500

505

510

act ggt tac atg ttt gga aaa ggg gtt tac ttt gcg gat atg ttc tcc
1706
Thr Gly Tyr Met Phe Gly Lys Gly Val Tyr Phe Ala Asp Met Phe Ser

515

520

525

aag agt gcg aac tat tgc tat gcc aac act ggc gct aat gat ggc gtt
1754
Lys Ser Ala Asn Tyr Cys Tyr Ala Asn Thr Gly Ala Asn Asp Gly Val

530

535

540

PCDMOD~11.TXT

ctg ctc ctc tgc gag gtt gct ttg gga gac atg aat gaa ctt ctg tat
1802
Leu Leu Leu Cys Glu Val Ala Leu Gly Asp Met Asn Glu Leu Leu Tyr

545 550 555

tca gat tat aac gcg gat aat cta ccc ccg gga aag cta agc aca aaa
1850
Ser Asp Tyr Asn Ala Asp Asn Leu Pro Pro Gly Lys Leu Ser Thr Lys

560 565 570

ggt gtg ggg aaa aca gca cca aac cca tca gag gct caa aca cta gaa
1898
Gly Val Gly Lys Thr Ala Pro Asn Pro Ser Glu Ala Gln Thr Leu Glu

575 580 585 590

gac ggt gtt gtt cca ctt ggc aaa cca gtg gaa cgt tca tgc tcc
1946
Asp Gly Val Val Val Pro Leu Gly Lys Pro Val Glu Arg Ser Cys Ser

595 600 605

aag ggg atg ttg ttg tac aac gaa tat ata gtc tac aat gtg gaa caa
1994
Lys Gly Met Leu Leu Tyr Asn Glu Tyr Ile Val Tyr Asn Val Glu Gln

610 615 620

atc aag atg cgt tat gtg atc caa gtc aaa ttc aac tac aag cac taa
2042
Ile Lys Met Arg Tyr Val Ile Gln Val Lys Phe Asn Tyr Lys His

625 630 635

aacttatgta tattagcttt tgaacatcaa ctaattatcc aaaaatcagc gttttatgt
2102

atttctttca aactccttca tctctgattt tgcacggttc actcg
2147

PCDMOD~11.TXT

<210> 6

<211> 637

<212> PRT

<213> *Arabidopsis thaliana*

<400> 6

Met Ala Asn Lys Leu Lys Val Asp Glu Leu Arg Leu Lys Leu Ala Glu
1 5 10 15

Arg Gly Leu Ser Thr Thr Gly Val Lys Ala Val Leu Val Glu Arg Leu
20 25 30

Glu Glu Ala Ile Ala Glu Asp Thr Lys Lys Glu Glu Ser Lys Ser Lys
35 40 45

Arg Lys Arg Asn Ser Ser Asn Asp Thr Tyr Glu Ser Asn Lys Leu Ile
50 55 60

Ala Ile Gly Glu Phe Arg Gly Met Ile Val Lys Glu Leu Arg Glu Glu
65 70 75 80

Ala Ile Lys Arg Gly Leu Asp Thr Thr Gly Thr Lys Lys Asp Leu Leu
85 90 95

Glu Arg Leu Cys Asn Asp Ala Asn Asn Val Ser Asn Ala Pro Val Lys
100 105 110

Ser Ser Asn Gly Thr Asp Glu Ala Glu Asp Asp Asn Asn Gly Phe Glu
115 120 125

Glu Glu Lys Lys Glu Glu Lys Ile Val Thr Ala Thr Lys Lys Gly Ala
130 135 140

PCDMOD~11.TXT

Ala Val Leu Asp Gln Trp Ile Pro Asp Glu Ile Lys Ser Gln Tyr His
145 150 155 160

Val Leu Gln Arg Gly Asp Asp Val Tyr Asp Ala Ile Leu Asn Gln Thr
165 170 175

Asn Val Arg Asp Asn Asn Lys Phe Phe Val Leu Gln Val Leu Glu
180 185 190

Ser Asp Ser Lys Lys Thr Tyr Met Val Tyr Thr Arg Trp Gly Arg Val
195 200 205

Gly Val Lys Gly Gln Ser Lys Leu Asp Gly Pro Tyr Asp Ser Trp Asp
210 215 220

Arg Ala Ile Glu Ile Phe Thr Asn Lys Phe Asn Asp Lys Thr Lys Asn
225 230 235 240

Tyr Trp Ser Asp Arg Lys Glu Phe Ile Pro His Pro Lys Ser Tyr Thr
245 250 255

Trp Leu Glu Met Asp Tyr Gly Lys Glu Glu Asn Asp Ser Pro Val Asn
260 265 270

Asn Asp Ile Pro Ser Ser Ser Glu Val Lys Pro Glu Gln Ser Lys
275 280 285

Leu Asp Thr Arg Val Ala Lys Phe Ile Ser Leu Ile Cys Asn Val Ser
290 295 300

Met Met Ala Gln His Met Met Glu Ile Gly Tyr Asn Ala Asn Lys Leu
305 310 315 320

Pro Leu Gly Lys Ile Ser Lys Ser Thr Ile Ser Lys Gly Tyr Glu Val
325 330 335

PCDMOD~11.TXT

Leu Lys Arg Ile Ser Glu Val Ile Asp Arg Tyr Asp Arg Thr Arg Leu
340 345 350

Glu Glu Leu Ser Gly Glu Phe Tyr Thr Val Ile Pro His Asp Phe Gly
355 360 365

Phe Lys Lys Met Ser Gln Phe Val Ile Asp Thr Pro Gln Lys Leu Lys
370 375 380

Gln Lys Ile Glu Met Val Glu Ala Leu Gly Glu Ile Glu Leu Ala Thr
385 390 395 400

Lys Leu Leu Ser Val Asp Pro Gly Leu Gln Asp Asp Pro Leu Tyr Tyr
405 410 415

His Tyr Gln Gln Leu Asn Cys Gly Leu Thr Pro Val Gly Asn Asp Ser
420 425 430

Glu Glu Phe Ser Met Val Ala Asn Tyr Met Glu Asn Thr His Ala Lys
435 440 445

Thr His Ser Gly Tyr Thr Val Glu Ile Ala Gln Leu Phe Arg Ala Ser
450 455 460

Arg Ala Val Glu Ala Asp Arg Phe Gln Gln Phe Ser Ser Ser Lys Asn
465 470 475 480

Arg Met Leu Leu Trp His Gly Ser Arg Leu Thr Asn Trp Ala Gly Ile
485 490 495

Leu Ser Gln Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly
500 505 510

Tyr Met Phe Gly Lys Gly Val Tyr Phe Ala Asp Met Phe Ser Lys Ser
515 520 525

PCDMOD~11.TXT

Ala Asn Tyr Cys Tyr Ala Asn Thr Gly Ala Asn Asp Gly Val Leu Leu
530 535 540

Leu Cys Glu Val Ala Leu Gly Asp Met Asn Glu Leu Leu Tyr Ser Asp
545 550 555 560

Tyr Asn Ala Asp Asn Leu Pro Pro Gly Lys Leu Ser Thr Lys Gly Val
565 570 575

Gly Lys Thr Ala Pro Asn Pro Ser Glu Ala Gln Thr Leu Glu Asp Gly
580 585 590

Val Val Val Pro Leu Gly Lys Pro Val Glu Arg Ser Cys Ser Lys Gly
595 600 605

Met Leu Leu Tyr Asn Glu Tyr Ile Val Tyr Asn Val Glu Gln Ile Lys
610 615 620

Met Arg Tyr Val Ile Gln Val Lys Phe Asn Tyr Lys His
625 630 635

<210> 7

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> A domain of non-conventional PARP proteins

<220>

<221> MISC_FEATURE

PCDMOD~11.TXT

<222> (3)..(3)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Xaa represents any amino acid

<220>

PCDMOD~11.TXT

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (12)..(12)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (13)..(13)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (14)..(14)

<223> Xaa represents any amino acid

PCDMOD~11.TXT

<400> 7

Arg Gly Xaa Xaa Xaa Xaa Gly Xaa Lys Xaa Xaa Xaa Xaa Arg Leu
1 5 10 15

<210> 8

<211> 33

<212> PRT

<213> Artificial sequence

<220>

<223> A1 domain of non-conventional PARP proteins

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa represents any amino acid

PCDMOD~11.TXT

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)

PCDMOD~11.TXT

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (13)..(13)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (18)..(18)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (19)..(19)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

PCDMOD~11.TXT

<222> (23)..(23)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (24)..(24)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (27)..(27)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (30)..(30)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (31)..(31)

<223> Xaa represents any amino acid

<400> 8

PCDMOD~11.TXT

Xaa Leu Xaa Val Xaa Xaa Xaa Arg Xaa Xaa Leu Xaa Xaa Arg Gly Leu
1 5 10 15

Xaa Xaa Xaa Gly Val Lys Xaa Xaa Leu Val Xaa Arg Leu Xaa Xaa Ala
20 25 30

Ile

<210> 9

<211> 30

<212> PRT

<213> Artificial sequence

<220>

<223> A2 domain of non-conventional PARP protein

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa represents any amino acid

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa represents any amino acid

<220>

PCDMOD~11.TXT

<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa represents any amino acid

PCDMOD~11.TXT

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (18)..(18)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> Xaa represents any amino acid

PCDMOD~11.TXT

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (25)..(25)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> Xaa represents any amino acid

<220>
<221> MISC_FEATURE
<222> (30)..(30)

PCDMOD~11.TXT

<223> Xaa represents any amino acid

<400> 9

Gly Met Xaa Xaa Xaa Glu Leu Xaa Xaa Xaa Ala Xaa Xaa Arg Gly Xaa
1 5 10 15

Xaa Xaa Xaa Gly Xaa Lys Lys Asp Xaa Xaa Arg Leu Xaa Xaa
20 25 30

<210> 10

<211> 3212

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (81)..(3020)

<223>

<400> 10

gcttcctctg tcgtccggcc tccaaactcca tcgaaggggc tagggagagg agggAACCCG
60

aaccacagca ggccggcgca atg gcg gcg ccg cca aag gcg tgg aag gcg gag
113

Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu...

1

5

10

tat gcc aag tct ggg cgg gcc tcg tgc aag tca tgc cgg tcc cct atc
161

Tyr Ala Lys Ser Gly Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile

PCDMOD~11.TXT

15

20

25

gcc aag gac cag ctc cgt ctt ggc aag atg gtt cag gcg tca cag ttc
209
Ala Lys Asp Gln Leu Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe

30

35

40

gac ggc ttc atg ccg atg tgg aac cat gcc agg tgc atc ttc agc aag
257
Asp Gly Phe Met Pro Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys

45

50

55

aag aac cag ata aaa tcc gtt gac gat gtt gaa ggg ata gat gca ctt
305
Lys Asn Gln Ile Lys Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu

60

65

70

75

aga tgg gat gat caa gag aag ata cga aac tac gtt ggg agt gcc tca
353
Arg Trp Asp Asp Gln Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser

80

85

90

gct ggt aca agt tct aca gct gct cct cct gag aaa tgt aca att gag
401
Ala Gly Thr Ser Ser Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu

95

100

105

att gct cca tct gcc cgt act tca tgt aga cga tgc agt gaa aag att
449
Ile Ala Pro Ser Ala Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile

110

115

120

aca aaa gga tcg gtc cgt ctt tca gct aag ctt gag agt gaa ggt ccc
497

PCDMOD~11.TXT

Thr Lys Gly Ser Val Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro

125

130

135

aag ggt ata cca tgg tat cat gcc aac tgt ttc ttt gag gta tcc ccg

545

Lys Gly Ile Pro Trp Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro

140

145

150

155

tct gca act gtt gag aag ttc tca ggc tgg gat act ttg tcc gat gag

593

Ser Ala Thr Val Glu Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu

160

165

170

gat aag aga acc atg ctc gat ctt gtt aaa aaa gat gtt ggc aac aat

641

Asp Lys Arg Thr Met Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn

175

180

185

gaa caa aat aag ggt tcc aag cgc aag aaa agt gaa aat gat att gat

689

Glu Gln Asn Lys Gly Ser Lys Arg Lys Ser Glu Asn Asp Ile Asp

190

195

200

agc tac aaa tcc gcc agg tta gat gaa agt aca tct gaa ggt aca gtg

737

Ser Tyr Lys Ser Ala Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val

205

210

215

cga aac aaa ggg caa ctt gta gac cca cgt ggt tcc aat act agt tca

785

Arg Asn Lys Gly Gln Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser

220

225

230

235

gct gat atc caa cta aag ctt aag gag caa agt gac aca ctt tgg aag

PCDMOD~11.TXT

833

Ala Asp Ile Gln Leu Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys

240

245

250

tta aag gat gga ctt aag act cat gta tcg gct gct gaa tta agg gat

881

Leu Lys Asp Gly Leu Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp

255

260

265

atg ctt gag gct aat ggg cag gat aca tca gga cca gaa agg cac cta

929

Met Leu Glu Ala Asn Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu

270

275

280

ttg gat cgc tgt gcg gat gga atg ata ttt gga gcg ctg ggt cct tgc

977

Leu Asp Arg Cys Ala Asp Gly Met Ile Phe Gly Ala Leu Gly Pro Cys

285

290

295

cca gtc tgt gct aat ggc atg tac tat tat aat ggt cag tac caa tgc

1025

Pro Val Cys Ala Asn Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys

300

305

310

315

agt ggt aat gtg tca gag tgg tcc aag tgt aca tac tct gcc aca gaa

1073

Ser Gly Asn Val Ser Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu

320

325

330

cct gtc cgc gtt aag aag aag tgg caa att cca cat gga aca aag aat

1121

Pro Val Arg Val Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn

335

340

345

PCDMOD~11.TXT

gat tac ctt atg aag tgg ttc aaa tct caa aag gtt aag aaa cca gag
1169
Asp Tyr Leu Met Lys Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu

350 355 360

agg gtt ctt cca cca atg tca cct gag aaa tct gga agt aaa gca act
1217
Arg Val Leu Pro Pro Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr

365 370 375

cag aga aca tca ttg ctg tct tct aaa ggg ttg gat aaa tta agg ttt
1265
Gln Arg Thr Ser Leu Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe

380 385 390 395

tct gtt gta gga caa tca aaa gaa gca gca aat gag ttg att gag aag
1313
Ser Val Val Gly Gln Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys

400 405 410

ctc aaa ctt gct ggt gcc aac ttc tat gcc agg gtt gtc aaa gat att
1361
Leu Lys Leu Ala Gly Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile

415 420 425

gat tgt tta att gca tgt ggt gag ctc gac aat gaa aat gct gaa gtc
1409
Asp Cys Leu Ile Ala Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val

430 435 440

agg aaa gca agg agg ctg aag ata cca att gta agg gag ggt tac att
1457
Arg Lys Ala Arg Arg Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile

445 450 455

PCDMOD~11.TXT

gga gaa tgt gtt aaa aag aac aaa atg ctg cca ttt gat ttg tat aaa
1505
Gly Glu Cys Val Lys Lys Asn Lys Met Leu Pro Phe Asp Leu Tyr Lys

460 465 470 475

cta gag aat gcc tta gag tcc tca aaa ggc agt act gtc act gtt aaa
1553
Leu Glu Asn Ala Leu Glu Ser Ser Lys Gly Ser Thr Val Thr Val Lys

480 485 490

gtt aag ggc cga agt gct gtt cat gag tcc tct ggt ttg caa gat act
1601
Val Lys Gly Arg Ser Ala Val His Glu Ser Ser Gly Leu Gln Asp Thr

495 500 505

gct cac att ctt gaa gat ggg aaa agc ata tac aat gca acc tta aac
1649
Ala His Ile Leu Glu Asp Gly Lys Ser Ile Tyr Asn Ala Thr Leu Asn

510 515 520

atg tct gac ctg gca cta ggt gtg aac agc tac tat gta ctc cag atc
1697
Met Ser Asp Leu Ala Leu Gly Val Asn Ser Tyr Tyr Val Leu Gln Ile

525 530 535

att gaa cag gat gat ggg tct gag tgc tac gta ttt cgt aag tgg gga
1745
Ile Glu Gln Asp Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly

540 545 550 555

cgg gtt ggg agt gag aaa att gga ggg caa aaa ctg gag gag atg tca
1793
Arg Val Gly Ser Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser

560 565 570

PCDMOD~11.TXT

aaa act gag gca atc aag gaa ttc aaa aga tta ttt ctt gag aag act
1841
Lys Thr Glu Ala Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr

575 580 585

gga aac tca tgg gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag
1889
Gly Asn Ser Trp Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln

590 595 600

cct ggg aga ttt tac cca ctt gat gtt gat tat ggt gtt aag aaa gca
1937
Pro Gly Arg Phe Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala

605 610 615

cca aaa cgg aaa gat atc agt gaa atg aaa agt tct ctt gct cct caa
1985
Pro Lys Arg Lys Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln

620 625 630 635

ttg cta gaa ctc atg aag atg ctt ttc aat gtg gag aca tat aga gct
2033
Leu Leu Glu Leu Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala

640 645 650

gct atg atg gaa ttt gaa att aat atg tca gaa atg cct ctt ggg aag
2081
Ala Met Met Glu Phe Glu Ile Asn Met Ser Glu Met Pro Leu Gly Lys

655 660 665

cta agc aag gaa aat att gag aaa gga ttt gaa gca tta act gag ata
2129
Leu Ser Lys Glu Asn Ile Glu Lys Gly Phe Glu Ala Leu Thr Glu Ile

PCDMOD~11.TXT

670

675

680

cag aat tta ttg aag gac acc gct gat caa gca ctg gct gtt aga gaa
2177

Gln Asn Leu Leu Lys Asp Thr Ala Asp Gln Ala Leu Ala Val Arg Glu

685

690

695

agc tta att gtt gct gcg agc aat cgc ttt ttc act ctt atc cct tct
2225

Ser Leu Ile Val Ala Ala Ser Asn Arg Phe Phe Thr Leu Ile Pro Ser

700

705

710

715

att cat cct cat att ata cgg gat gag gat gat ttg atg atc aaa gcg
2273

Ile His Pro His Ile Ile Arg Asp Glu Asp Asp Leu Met Ile Lys Ala

720

725

730

aaa atg ctt gaa gct ctg cag gat att gaa att gct tca aag ata gtt
2321

Lys Met Leu Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val

735

740

745

ggc ttc gat agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa
2369

Gly Phe Asp Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys

750

755

760

ctt cac tgt gac atc acc ccg ctg gct cac gat agt gaa gat tac aag
2417

Leu His Cys Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys

765

770

775

tta att gag cag tat ctc ctc aac aca cat gct cct act cac aag gac
2465

Leu Ile Glu Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp

PCDMOD~11.TXT

780 785 790 795

tgg tcg ctg gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa
2513
Trp Ser Leu Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu

800 805 810

ctt aat aag tac tca aga tat aaa aat aat ctg cat aac aag atg cta
2561
Leu Asn Lys Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu

815 820 825

tta tgg cac ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa
2609
Leu Trp His Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln

830 835 840

ggg cta aga att gca cct cct gag gca cct gtt act ggc tat atg ttc
2657
Gly Leu Arg Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe

845 850 855

ggc aaa ggc ctc tac ttt gca gat cta gta agc aag agc gca caa tac
2705
Gly Lys Gly Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr

860 865 870 875

tgt tat gtg gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag
2753
Cys Tyr Val Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu

880 885 890

gtt gct tta gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac
2801

PCDMOD~11.TXT

Val Ala Leu Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp

895

900

905

aaa cct cca aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg
2849

Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val

910

915

920

cca ctg gag tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc
2897

Pro Leu Glu Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro

925

930

935

tgc ggc aag ccg gtg cca tca tca att agg agc tct gaa ctc atg tac
2945

Cys Gly Lys Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr

940

945

950

955

aat gag tac atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg
2993

Asn Glu Tyr Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu

960

965

970

ctg aag gtg cgt ttc cat cac aag agg tagctggag actaggcaag
3040

Leu Lys Val Arg Phe His His Lys Arg

975

980

tagagttgga aggttagagaa gcagagttag gcgatgcctc ttttggatt attagtaagc
3100

ctggcatgta ttatgggtg ctcgcgttg atccatttg gtaagtgttgc ttgggcatc
3160

agcgcgata gcaccaatca cacacttta cctaatgacg tttactgta ta
3212

PCDMOD~11.TXT

<210> 11

<211> 980

<212> PRT

<213> Zea mays

<400> 11

Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
1 5 10 15

Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
20 25 30

Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
35 40 45

Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
50 55 60

Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
65 70 75 80

Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
85 90 95

Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
100 105 110

Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
115 120 125

Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
130 135 140

PCDMOD~11.TXT

Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
145 150 155 160

Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
165 170 175

Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
180 185 190

Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
195 200 205

Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
210 215 220

Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
225 230 235 240

Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
245 250 255

Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
260 265 270

Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
275 280 285

Asp Gly Met Ile Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
290 295 300

Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
305 310 315 320

Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
325 330 335

PCDMOD~11.TXT

Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
340 345 350

Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
355 360 365

Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
370 375 380

Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
385 390 395 400

Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
405 410 415

Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
420 425 430

Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
435 440 445

Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
450 455 460

Lys Asn Lys Met Leu Pro Phe Asp Leu Tyr Lys Leu Glu Asn Ala Leu
465 470 475 480

Glu Ser Ser Lys Gly Ser Thr Val Thr Val Lys Val Lys Gly Arg Ser
485 490 495

Ala Val His Glu Ser Ser Gly Leu Gln Asp Thr Ala His Ile Leu Glu
500 505 510

Asp Gly Lys Ser Ile Tyr Asn Ala Thr Leu Asn Met Ser Asp Leu Ala
515 520 525

PCDMOD~11.TXT

Leu Gly Val Asn Ser Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp Asp
530 535 540

Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser Glu
545 550 555 560

Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala Ile
565 570 575

Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp Glu
580 585 590

Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe Tyr
595 600 605

Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys Asp
610 615 620

Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu Met
625 630 635 640

Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu Phe
645 650 655

Glu Ile Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Lys Glu Asn
660 665 670

Ile Glu Lys Gly Phe Glu Ala Leu Thr Glu Ile Gln Asn Leu Leu Lys
675 680 685

Asp Thr Ala Asp Gln Ala Leu Ala Val Arg Glu Ser Leu Ile Val Ala
690 695 700

Ala Ser Asn Arg Phe Phe Thr Leu Ile Pro Ser Ile His Pro His Ile
705 710 715 720

PCDMOD~11.TXT

Ile Arg Asp Glu Asp Asp Leu Met Ile Lys Ala Lys Met Leu Glu Ala
725 730 735

Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp Ser Asp
740 745 750

Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys Asp Ile
755 760 765

Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu Gln Tyr
770 775 780

Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu Glu Leu
785 790 795 800

Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys Tyr Ser
805 810 815

Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His Gly Ser
820 825 830

Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg Ile Ala
835 840 845

Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly Leu Tyr
850 855 860

Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val Asp Arg
865 870 875 880

Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu Gly Asp
885 890 895

Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro Arg Gly
900 905 910

PCDMOD~11.TXT

Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu Ser Glu
915 920 925

Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys Pro Val
930 935 940

Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr Ile Val
945 950 955 960

Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val Arg Phe
965 970 975

His His Lys Arg
980

<210> 12

<211> 1010

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein between APP N-terminal domain and GUS protein

<400> 12

Met Ala Asn Lys Leu Lys Val Asp Glu Leu Arg Leu Lys Leu Ala Glu
1 5 10 15

Arg Gly Leu Ser Thr Thr Gly Val Lys Ala Val Leu Val Glu Arg Leu
20 25 30

Glu Glu Ala Ile Ala Glu Asp Thr Lys Lys Glu Glu Ser Lys Ser Lys
35 40 45

PCDMOD~11.TXT

Arg Lys Arg Asn Ser Ser Asn Asp Thr Tyr Glu Ser Asn Lys Leu Ile
50 55 60

Ala Ile Gly Glu Phe Arg Gly Met Ile Val Lys Glu Leu Arg Glu Glu
65 70 75 80

Ala Ile Lys Arg Gly Leu Asp Thr Thr Gly Thr Lys Lys Asp Leu Leu
85 90 95

Glu Arg Leu Cys Asn Asp Ala Asn Asn Val Ser Asn Ala Pro Val Lys
100 105 110

Ser Ser Asn Gly Thr Asp Glu Ala Glu Asp Asp Asn Asn Gly Phe Glu
115 120 125

Glu Glu Lys Lys Glu Glu Lys Ile Val Thr Ala Thr Lys Lys Gly Ala
130 135 140

Ala Val Leu Asp Gln Trp Ile Pro Asp Glu Ile Lys Ser Gln Tyr His
145 150 155 160

Val Leu Gln Arg Gly Asp Asp Val Tyr Asp Ala Ile Leu Asn Gln Thr
165 170 175

Asn Val Arg Asp Asn Asn Asn Lys Phe Phe Val Leu Gln Val Leu Glu
180 185 190

Ser Asp Ser Lys Lys Thr Tyr Met Val Tyr Thr Arg Trp Gly Arg Val
195 200 205

Gly Val Lys Gly Gln Ser Lys Leu Asp Gly Pro Tyr Asp Ser Trp Asp
210 215 220

Arg Ala Ile Glu Ile Phe Thr Asn Lys Phe Asn Asp Lys Thr Lys Asn
225 230 235 240

PCDMOD~11.TXT

Tyr Trp Ser Asp Arg Lys Glu Phe Ile Pro His Pro Lys Ser Tyr Thr
245 250 255

Trp Leu Glu Met Asp Tyr Gly Lys Glu Glu Asn Asp Ser Pro Val Asn
260 265 270

Asn Asp Ile Pro Ser Ser Ser Glu Val Lys Pro Glu Gln Ser Lys
275 280 285

Leu Asp Thr Arg Val Ala Lys Phe Ile Ser Leu Ile Cys Asn Val Ser
290 295 300

Met Met Ala Gln His Met Met Glu Ile Gly Tyr Asn Ala Asn Lys Leu
305 310 315 320

Pro Leu Gly Lys Ile Ser Lys Ser Thr Ile Ser Lys Gly Tyr Glu Val
325 330 335

Leu Lys Arg Ile Ser Glu Val Ile Asp Arg Tyr Asp Arg Thr Arg Leu
340 345 350

Glu Glu Leu Ser Gly Glu Phe Tyr Thr Val Ile Pro His Asp Phe Gly
355 360 365

Phe Lys Lys Met Ser Gln Phe Val Ile Asp Thr Pro Gln Lys Leu Lys
370 375 380

Gln Lys Ile Glu Met Val Glu Ala Leu Gly Glu Ile Glu Leu Ala Thr
385 390 395 400

Lys Leu Leu Ser Val Asp Pro Met Val Arg Pro Val Glu Thr Pro Thr
405 410 415

Arg Glu Ile Lys Lys Leu Asp Gly Leu Trp Ala Phe Ser Leu Asp Arg
420 425 430

PCDMOD~11.TXT

Glu Asn Cys Gly Ile Asp Gln Arg Trp Trp Glu Ser Ala Leu Gln Glu
435 440 445

Ser Arg Ala Ile Ala Val Pro Gly Ser Phe Asn Asp Gln Phe Ala Asp
450 455 460

Ala Asp Ile Arg Asn Tyr Ala Gly Asn Val Trp Tyr Gln Arg Glu Val
465 470 475 480

Phe Ile Pro Lys Gly Trp Ala Gly Gln Arg Ile Val Leu Arg Phe Asp
485 490 495

Ala Val Thr His Tyr Gly Lys Val Trp Val Asn Asn Gln Glu Val Met
500 505 510

Glu His Gln Gly Gly Tyr Thr Pro Phe Glu Ala Asp Val Thr Pro Tyr
515 520 525

Val Ile Ala Gly Lys Ser Val Arg Ile Thr Val Cys Val Asn Asn Glu
530 535 540

Leu Asn Trp Gln Thr Ile Pro Pro Gly Met Val Ile Thr Asp Glu Asn
545 550 555 560

Gly Lys Lys Lys Gln Ser Tyr Phe His Asp Phe Phe Asn Tyr Ala Gly
565 570 575

Ile His Arg Ser Val Met Leu Tyr Thr Thr Pro Asn Thr Trp Val Asp
580 585 590

Asp Ile Thr Val Val Thr His Val Ala Gln Asp Cys Asn His Ala Ser
595 600 605

Val Asp Trp Gln Val Val Ala Asn Gly Asp Val Ser Val Glu Leu Arg
610 615 620

PCDMOD~11.TXT

Asp Ala Asp Gln Gln Val Val Ala Thr Gly Gln Gly Thr Ser Gly Thr
625 630 635 640

Leu Gln Val Val Asn Pro His Leu Trp Gln Pro Gly Glu Gly Tyr Leu
645 650 655

Tyr Glu Leu Cys Val Thr Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr
660 665 670

Pro Leu Arg Val Gly Ile Arg Ser Val Ala Val Lys Gly Glu Gln Phe
675 680 685

Leu Ile Asn His Lys Pro Phe Tyr Phe Thr Gly Phe Gly Arg His Glu
690 695 700

Asp Ala Asp Leu Arg Gly Lys Gly Phe Asp Asn Val Leu Met Val His
705 710 715 720

Asp His Ala Leu Met Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser
725 730 735

His Tyr Pro Tyr Ala Glu Glu Met Leu Asp Trp Ala Asp Glu His Gly
740 745 750

Ile Val Val Ile Asp Glu Thr Ala Ala Val Gly Phe Asn Leu Ser Leu
755 760 765

Gly Ile Gly Phe Glu Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu
770 775 780

Glu Ala Val Asn Gly Glu Thr Gln Gln Ala His Leu Gln Ala Ile Lys
785 790 795 800

Glu Leu Ile Ala Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser
805 810 815

PCDMOD~11.TXT

Ile Ala Asn Glu Pro Asp Thr Arg Pro Gln Gly Ala Arg Glu Tyr Phe
820 825 830

Ala Pro Leu Ala Glu Ala Thr Arg Lys Leu Asp Pro Thr Arg Pro Ile
835 840 845

Thr Cys Val Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile Ser
850 855 860

Asp Leu Phe Asp Val Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val
865 870 875 880

Gln Ser Gly Asp Leu Glu Thr Ala Glu Lys Val Leu Glu Lys Glu Leu
885 890 895

Leu Ala Trp Gln Glu Lys Leu His Gln Pro Ile Ile Ile Thr Glu Tyr
900 905 910

Gly Val Asp Thr Leu Ala Gly Leu His Ser Met Tyr Thr Asp Met Trp
915 920 925

Ser Glu Glu Tyr Gln Cys Ala Trp Leu Asp Met Tyr His Arg Val Phe
930 935 940

Asp Arg Val Ser Ala Val Val Gly Glu Gln Val Trp Asn Phe Ala Asp
945 950 955 960

Phe Ala Thr Ser Gln Gly Ile Leu Arg Val Gly Gly Asn Lys Lys Gly
965 970 975

Ile Phe Thr Arg Asp Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu Gln
980 985 990

Lys Arg Trp Thr Gly Met Asn Phe Gly Glu Lys Pro Gln Gln Gly Gly
995 1000 1005

PCDMOD~11.TXT

Lys Gln
1010

<210> 13

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> degenerated PCR primer

<220>

<221> misc_feature

<222> (11)..(11)

<223> n represents a,g,c or t

<220>

<221> misc_feature

<222> (23)..(23)

<223> n represents a,g,c or t

<400> 13
ccgaattcgg ntayatgtt y ggnaa
25

<210> 14

<211> 25

PCDMOD~11.TXT

<212> DNA
<213> Artificial sequence

<220>
<223> degenerated PCR primer

<220>
<221> misc_feature
<222> (11)..(11)
<223> n represents a, g, c or t

<400> 14
ccgaattcac natrtaytcr ttrta
25

<210> 15
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide for use as PCR primer
<400> 15
gggaccatgt agtttatctt gacct
25

<210> 16
<211> 26

PCDMOD~11.TXT

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide for use in PCR

<400> 16

gacctcgtag cccaaactctt ccccat

26

<210> 17

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide for use in PCR

<400> 17

aagtgcacgc ggccgccaca cctagtgcca ggtcag

36

<210> 18

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide for use in PCR

PCDMOD~11.TXT

<400> 18
atctcaattg tacatttctc agga
24

<210> 19

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide for use in PCR

<400> 19
aggatcccat ggcgaacaag ctc当地gta c
31

<210> 20

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide for use in PCR

<400> 20
aggatcctta gtgctttag ttgaat
26

<210> 21

<211> 4947

PCDMOD~11.TXT

<212> DNA

<213> Artificial sequence

<220>

<223> APP promoter fusion with beta-glucuronidase gene

<220>

<221> promoter

<222> (1)..(1961)

<223>

<220>

<221> misc_feature

<222> (1962)..(1964)

<223> translation initiation codon

<220>

<221> misc_feature

<222> (3795)..(3795)

<223> n represents a,c,g or t

....<220>

<221> misc_feature

<222> (3796)..(3796)

<223> n represents a,c,g or t

PCDMOD~11.TXT

<220>
<221> misc_feature
<222> (3797) .. (3797)
<223> n represents a,c,g or t

<220>
<221> misc_feature
<222> (3798) .. (3798)
<223> n represents a,c,g or t

<220>
<221> misc_feature
<222> (3799) .. (3799)
<223> n represents a,c,g or t

<220>
<221> misc_feature
<222> (3800) .. (3800)
<223> n represents a,c,g or t

<400> 21
ctcgagatag tatatttttt agttactatc attacataag tatatttaa aaaactaatt
60

atatgaatta tgtagctaac tagatagata atcgtataac caattcatgt tagtatagt
120

PCDMOD~11.TXT

tagtttaagt atgtattttg ggattacaag tgtggttggc atcaagacaa ggatgggtat
180

agcctttctc tgtaatttgg tttaaaaaaa gttttgcat tttatgtata aacgtgttt
240

tttttataa tttcaaattt caacaaaaaa caatttttt taataatgtat tgaccactat
300

agacaattt aatgataaaaa aaaagggggaa attttcaca atgtttgga gattagtcta
360

gatttttgc ccaaattttc cgattgtaag aattaagaag caatgaacat ttgtgttaag
420

cttaatgatt tgtactcaca atatctttt aatttaaaat tgttaaccaa aatatcctat
480

atattgtact tgtaatagaa atataaacta ttaaaaacaa cactttattc atataatata
540

agttaaaaca tatgttttt ttagtatgtt ctaatcacac ctattaaaaa aagttgaagc
600

taaatgagcc aaaaagaaaaa ataaagatag gggatggggaa caggctgtaa tggtaggcgg
660

ttggtatatg aactgagaac atgtctgttg gttcggtcca tctacgccac tcaaccattt
720

ggctatgtt tcttttggc ttttgcattt tctctctact tttttttttt ggtcaaaatc
780

tctatctcgt cttttacatg gcttacccga atgttagttt tcatgtaaat ttggttatga
840

aaagatattt tatataaact ttatcgata ttaatatcgt tatcatctaa ccattttta
900

aaactaaact agaaccatcc agtttacaa gagttttttttttttttttc taactaaata
960

atatttgaag tgtacaatat taacaatata tgggccaaat aatagtggaa accaaatcgt
1020

tagcccaact ttatgatggg cctgttgatt cttatgtctt ctgcgttgtt tttttttttt
1080

PCDMOD~11.TXT

cagattacgg gctaataaac atgcatgttt agttttact gtccaagtaa cgaatttta
1140

tctttgggt tggtggccca tttcatatat tccaaatgcc aaatccagcc cggtcgaca
1200

cagcactgct cggtcaaca ctcgtatgct gttggtagcc acttaagacc ttggtttgc
1260

taacatgtta cgaataattt gtgtcccttt ttcttcaagg agactaatct cttaataaa
1320

aaaagaattt tgtcattagt caacacaagt cctataatcc gtttacgtaa tttgtatgca
1380

cgtccttggaa aaagttagt gtggcgtagt ttacagccaa aaactatttgc tatattttct
1440

ttcgtaaac aaccagccaa attttcagaa aaatgttctt aaattataaa ttagtagtac
1500

attttaaaac atagagattt tttgttctt ttaatagaag agttaaacct atgtacaaaa
1560

tttcaactcc tttcaaaagt atttgctgt tactagattt ttaacctttt ttttttatac
1620

tttcatgatt ttctattgt tgccatcatc aatggtagga aataaataact atttaaaaaa
1680

ggtcaggggt ggatttaaga atcaatccaa aagttgggg tctttggag attaaaaaagt
1740

tatatggaa atatccacaa atatgaacga gaactttgt caaaaaaatt taaaataatt
1800

tttcaaaaag ccctaaagct ttcaagggaa gccatcgatg aagaagaaaa cgaagaagaa
1860

gactttcaa acgttcgcgc gaactcactt ctgacgaaaa ccataacttcc tcagtcata
1920

tcccttccg acgaactatt ctcctgaaga agaagacgaa aatggcgaac aagctcaaag
1980

tcgacatggt ccgtcctgta gaaaccccaa cccgtgaaat caaaaaactc gacggcctgt
2040

PCDMOD~11.TXT

gggcattcag tctggatcgc gaaaactgtg gaattgatca gcgttggtgg gaaagcgcgt
2100

tacaagaaag ccggcaatt gctgtgccag gcagtttaa cgatcagttc gccgatgcag
2160

atattcgtaa ttatgcggc aacgtctggt atcagcgcga agtctttata ccgaaagggt
2220

ggcaggcca gcgtatcgtg ctgcgttcg atgcggtcac tcattacggc aaagtgtgg
2280

tcaataatca ggaagtgtatg gagcatcagg gcggctatac gccatttgaa gccgatgtca
2340

cgcgtatgt tattgccggg aaaagtgtac gtatcaccgt ttgtgtgaac aacgaactga
2400

actggcagac tatccgcgg ggaatgggtga ttaccgacga aaacggcaag aaaaagcagt
2460

cttacttcca tgatttcttt aactatgcgg gaatccatcg cagcgtaatg ctctacacca
2520

cggcaacac ctgggtggac gatatoaccg tggtgacgca tgcgcgcaa gactgttaacc
2580

acgcgtctgt tgactggcag gtgggtggcca atgggtatgt cagcgttgaa ctgcgtatg
2640

cggatcaaca ggtgggttgca actggacaag gcactagcgg gactttgcaa gtgggtgaatc
2700

cgcacctctg gcaaccgggt gaaggttatc tctatgaact gtgcgtcaca gccaaaagcc
2760

agacagagtg tgatatctac ccgcttcgac tcggcatccg gtcagtggca gtgaagggcg
2820

aacagttcct gattaaccac aaaccgttct actttactgg ctttggtcgt catgaagatg
2880

cggaacttacg tggcaaagga ttcgataacg tgctgatggt gcacgaccac gcattaatgg
2940

actggattgg ggccaactcc taccgtaccc cgcattaccc ttacgctgaa gagatgctcg
3000

PCDMOD~11.TXT

actggcaga tgaacatggc atcgtggtga ttgatgaaac tgctgctgtc ggcttaacc
3060

tctctttagg cattggttc gaagcggca acaagccaa agaactgtac agcgaagagg
3120

cagtcaacgg ggaaactcag caagcgcact tacaggcgat taaagagctg atagcgcgtg
3180

acaaaaaacca cccaagcgtg gtgatgtgga gtattgcca cgaaccggat acccgccgc
3240

aagtgcacgg gaatatttcg ccactggcg aagcaacgca taaactcgac ccgacgcgtc
3300

cgatcacctg cgtcaatgta atgttctgcg acgctcacac cgataccatc agcgatctct
3360

ttgatgtgct gtgcctgaac cgttattacg gatggtatgt ccaaagcggc gatttgaaa
3420

cggcagagaa ggtactggaa aaagaacttc tggcctggca ggagaaaactg catcagccga
3480

ttatcatcac cgaatacggc gtggatacgt tagccggct gcactcaatg tacaccgaca
3540

tgtggagtga agagtatcag tgtgcattggc tggatatgta tcaccgcgtc tttgatcg
3600

tcagcgccgt cgtcggtaaa caggtatgga atttcggca ttttgcgacc tcgcaaggca
3660

tattgcgcgt tggcggtaac aagaaaggaa tcttcactcg cgaccgcaaa ccgaagtccg
3720

cggctttct gctgcaaaaaa cgctggactg gcatgaactt cggtaaaaaa ccgcagcagg
3780

gaggcaaaca atgannnnn gaattggtcc tgcttaatg agatatgca gacgcata
3840

atcgcatgat atttgcttca aattctgttg tgcacgttgt aaaaaacctg agcatgtga
3900

gctcagatcc ttaccggccgg ttccggttca ttctaatgaa tatatcaccc gttactatcg
3960

PCDMOD~11.TXT

tatTTTatg aataatattc tccgttcaat ttactgattg taccctacta cttatatgta
4020
caatattaaa atgaaaacaa tatattgtgc tgaataggtt tatagcgaca tctatgatag
4080
agcgccacaa taacaaacaa ttgcgttta ttattacaaa tccaatttta aaaaaagcgg
4140
cagaaccggt caaacctaaa agactgatta cataaatctt attcaaattt caaaaggccc
4200
caggggctag tatctacgac acaccgagcg gcgaactaat aacgttcact gaagggaact
4260
ccgggtcccc gccggcgcbc atgggtgaga ttccttgaag ttgagtattt gccgtccgct
4320
ctaccgaaag ttacgggcac cattcaaccc ggtccagcac ggccggccggg taaccgactt
4380
gctggcccgaa gaattatgca gcattttttt ggtgtatgtg ggccccaaat gaagtgcagg
4440
tcaaacccttg acagtgacga caaatcggtt ggcgggtcca gggcgaattt tgcgacaaca
4500
tgtcgaggct cagcaggact ctagaggatc cccgggtacc gagctcaat tcactggccg
4560
tcgtttaca acgtcggtac tggaaaacc ctggcggtac ccaacttaat cgcccttgcag
4620
cacatcccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat cgcccttccc
4680
aacagttgcg cagcctgaat ggcgaatggc gcctgatgcg gtatTTTctc cttacgcac
4740
tgtcggtat ttacacccgc atatggtgca ctctcaggtac aatctgctct gatgccgcat
4800
agttaaGCCa gccccgacac cggccaaacac cggctgacgc gcccgtacgg gtttgtctgc
4860
tccccggcatc cgcttacaga caagctgtga cggctccgg gagctgcattt tgctcagaggt
4920

PCDMOD~11.TXT

tttcaccgta atcaccgaaa cgcgcg
4947